this would not reflect a substitution of serine by asparagine but rather a change to a threonine residue (ACT). We think that the data presented by Zhang and co-workers allow for either of the following conclusions: Either nucleotide position two at codon 63 in SSH1 is (highly) polymorphic and, therefore, S63N reflects an innocuous polymorphism rather than a true mutation. Or the authors erroneously show a different part of this patient's genome, but not the relevant heterozygous DNA sections necessary to support their previous notion that S63N is indeed causative in DSAP and their current assumption that these data indicate somatic LOH in this patient suffering from DSAP. Further we cannot see the relevance of performing LOH studies in DSAP by looking for the promotor transition c.−804G→A in *ARPC3*, considering that the authors themselves state in a previous publication that this nucleotide change was not only observed in affected individuals from family 2 but also in healthy control individuals (Zhang *et al*., 2005a), thus indicating that it is a common polymorphism rather than a mutation causing DSAP.

CONFLICT OF INTEREST

The authors state no conflict of interest.

ACKNOWLEDGMENTS

J.F. is member of the Network for Ichthyoses and Related Keratinization Disorders (NIRK) that is supported by the German Federal Ministry of Education and Research (BMBF). MAMvS is supported by grants from the GROW research institute of the University Hospital Maastricht, the La Roche Posay Research Foundation, and Barrier Therapeutics NV.

Jorge Frank[1], Michel van Geel[1] and Maurice A.M. van Steensel[1]

[1]Department of Dermatology and Maastricht University Centre for Molecular Dermatology (MUCMD), University Hospital Maastricht, Maastricht, The Netherlands
E-mail: jfra@sder.azm.nl

REFERENCES

Wei S, Yang S, Lin D, Li M, Zhang X, Bu L *et al.* (2004) A novel locus for disseminated superficial porokeratosis maps to chromosome 18p11.3. *J Invest Dermatol* 123:872–5

Xia K, Deng H, Xia JH, Zheng D, Zhang HL, Lu CY *et al.* (2002) A novel locus (DSAP2) for disseminated superficial actinic porokeratosis maps to chromosome 15q25.1–26.1. *Br J Dermatol* 147:650–4

Zhang Z, Niu Z, Yuan W, Liu W, Xiang L, Zhang J *et al.* (2004) Fine mapping and identification of a candidate gene *SSH1* in disseminated superficial actinic porokeratosis. *Hum Mutat* 24:438

Zhang ZH, Huang W, Niu ZM, Liu WD, Xiang LH, Yuan WT *et al.* (2005a) Two closely linked variations in actin cytoskeleton pathway in a Chinese pedigree with disseminated superficial actinic porokeratosis. *J Am Acad Dermatol* 52:972–6

Zhang ZH, Niu ZM, Huang W, Xiang LH, Gu CY, Yang L *et al.* (2006) Loss of heterozygosity analysis on chromosome 12q in disseminated superficial actinic porokeratosis. *J Invest Dermatol* 127:482–5

Zhang ZH, Niu ZM, Yuan WT, Zhao JJ, Jiang FX, Zhang J *et al.* (2005b) A mutation in *SART3* gene in a Chinese pedigree with disseminated superficial actinic porokeratosis. *Br J Dermatol* 152:658–63

Zhang ZH, Niu ZM, Yuan WT, Zhao JJ, Jiang FX, Zhang J *et al.* (2005c) Refinement of DSAP1 locus and mutation detection for candidate genes. *Yi Chuan Xue Bao* 32:667–74

Response to Loss of Heterozygosity Studies on Chromosome 12q in Disseminated Superficial Actinic Porokeratosis: Lessons to be Learned

Journal of Investigative Dermatology (2007) **127,** 2059–2060; doi:10.1038/sj.jid.5700784; published online 5 July 2007

TO THE EDITOR

To our knowledge, few groups focus on the study of disseminated superficial actinic porokeratosis (DSAP) etiopathogenesis, and they have not reported the candidate genes of DSAP. Our results confirmed the research of other groups, and we also found variations of the SSH1, ARPC3, and SART3 genes. Because we have found no reports about the gene causing DSAP, we published our findings hoping to learn other researcher's responses. Although Frank *et al.* (2007) raised strong doubts about our results, we are glad to discuss our study.

We never confirmed in our papers that SSH1, ARPC3, or SART3 are the genes causing DSAP; at this time, we have reported three candidate genes for DSAP. Like Frank *et al.* we are puzzled why no other researchers have reported on the disease gene, whether it is SSH1 or not.

In our papers, we suggest that SSH1, ARPC3, or SART3 are candidate genes, not the genes causing DSAP. In 12q23.2–24.1, there may be only one gene causing DSAP, but that does not

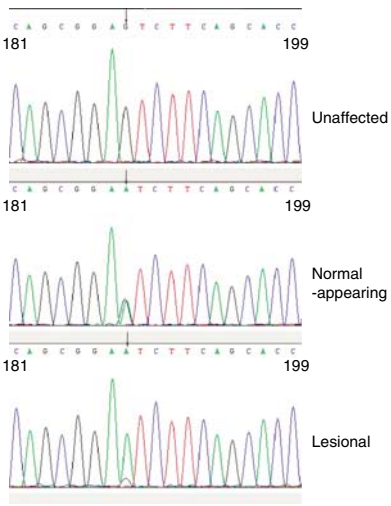

Figure 1. Chromatograms of the normal and mutated sequences and LOH in two affected members in Family 2. (**a**) NM_018984.2: c.188G>A (p.Ser63Asn) at *SSH1*.

necessarily mean there is only one candidate gene. We do not know whether SSH1, ARPC3, and SART3 are involved in the same pathway, but some papers suggest that SSH1 and ARPC3 may be involved in the actin cytoskeleton pathway (Welch *et al.*, 1997; Pollard *et al.*, 2000; Volkmann *et al.*, 2001; Niwa *et al.*, 2002; Pelham and Chang, 2002).

As to the heterozygous C/A-peak perhaps it is caused by the low-resolution online image referred to (Figure 1 which is reproduced here). We are not sure whether the S63N mutation is innocuous or not, but it should be confirmed by experiments.

We sincerely thank the authors for their attention to our research. The conclusions in our papers may be not perfect, but the data generated by the experiment are valid.

CONFLICT OF INTEREST

The author states no conflict of interest.

***Zhenghua Zhang*[1]**

[1]*Department of Dermatology, Huashan Hospital, Fudan University, Shanghai, PR China E-mail: verzhang@gmail.com*

REFERENCES

Frank J, van Geel M, van Steensel MAM (2007) Loss of heterozygosity studies on chromosome 12q in disseminated superficial active porokeratosis: lessons to be learned. *J Invest Dermatol* 127:2058–9

Niwa R, Nagata-Ohashi K, Takeichi M, Mizuno K, Uemura T (2002) Control of actin reorganization by Slingshot a family of phosphatases that dephosphorylate ADF/cofilin. *Cell* 108: 233–46

Pollard TD, Blanchoin L, Mullins RD (2000) Molecular mechanisms controlling actin filament dynamics in nonmuscle cells. *Annu Rev Biophys Biomol Struct* 29: 545–76

Pelham RJ, Chang F (2002) Actin dynamics in the contractile ring during cytokinesis in fission yeast. *Nature* 419:82–6

Volkmann N, Amann KJ, Stoilova-McPhie S, Egile C, Winter DC, Hazelwood L *et al.* (2001) Structure of Arp2/3 complex in its activated state and in actin filament branch junctions. *Science* 293:2456–9

Welch MD, DePace AH, Verma S, Iwamatsu A, Mitchison TJ (1997) The human Arp2/3 complex is composed of evolutionarily conserved subunits and is localized to cellular regions of dynamic actin filament assembly. *J Cell Biol* 138:375–84

Editor's Note

Journal of Investigative Dermatology (2007) **127,** 2060; doi:10.1038/sj.jid.5700955; published online 5 July 2007

TO THE EDITOR

An Associate Editor with expertise in the field reviewed the online publication in question, along with an independent observer, and agrees with Dr Zhang. In addition, the Editor reviewed all figures associated with this publication, including those submitted for review purposes and those published online and in print, and the Editor agrees with Dr Zhang. The Editor appreciates the concern over the validity of original data published in the *JID*, and considers this case closed.

Lowell A. Goldsmith

Editor

A Novel Mutation in K6b in Pachyonychia Congenita Type 2

Journal of Investigative Dermatology (2007) **127,** 2060–2062; doi:10.1038/sj.jid.5700814; published online 12 April 2007

TO THE EDITOR

Pachyonychia congenita is a rare autosomal-dominant disorder of keratin that was first described in 1685 (Leachman *et al.*, 2005). Named by Jadassohn and Lewandowsky in 1906, this syndrome is characterized by hypertrophic nail dystrophy, focal palmoplantar keratoderma, follicular keratoses, and other ectodermal features varying by subtype. It is now well known that pachyonychia congenita type 1 (PC-1), also known as Jadassohn–Lewandowsky syndrome, is caused by mutations in either keratin 6a (K6a) or keratin 16 (K16), whereas pachyonychia congenita type 2 (PC-2), also known as Jackson–Lawler syndrome, is caused by mutations in keratin 6b (K6b) or its expression partner keratin 17 (K17) (Munro, 2001). Both subtypes have hypertrophic nail dystrophy and painful plantar keratoderma as the most significant clinical findings with features such as natal teeth, steatocysts, and hair abnormalities being more common in PC-2 and oral leukokeratosis more common in pachyonychia congenita type 1 (Leachman *et al.*, 2005).

The number of patients worldwide that are believed to have PC is between 1,000 and 10,000 (Kaspar, 2005). There have been more than 82 mutations published in the literature thus far with all established mutations consistent

Abbreviations: K6a, keratin 6a; K6b, keratin 6b; K16, keratin 16; K17, keratin 17; PC-1, pachyonychia congenita type 1; PC-2, pachyonychia congenita type 2